

ALIGNMENT #4

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Qy      368 HisGlnLysGlyLysAspGluGlyValValTyrSerValValHisArgThrSerLysArg 387
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Db      1081 CACCAGAAAGGGAAGATGAAGGTGTTGCTACTCTGTGGTGCATAGAACCTCAAAGAGG 1140

Qy      388 SerGluAlaArgSerAlaGluPheThrValGlyArgLysAspSerSerIleIleCysAla 407
          |||
Db      1141 AGTGAAGCCAGGTCGTGCTGAGTTCACCGTGGGGAGAAAGGACAGTTCTATCATCTGTGCG 1200

Qy      408 GluValArgCysLeuGlnProSerGluValSerSerThrGluValAsnMetArgSerArg 427
          |||
Db      1201 GAGGTGAGATGCCTGCAGCCAGTCAGGTTTCATCCACGAGGTGAATATGAGAAGCAGG 1260

Qy      428 ThrLeuGlnGluProLeuSerAspCysGluGluValLeuCys 441
          |||
Db      1261 ACTCTCCAAGAACCCCTTAGCGACTGTGAGGAGGTTCTCTGC 1302

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RESULT 5

DJ447641

LOCUS DJ447641 1997 bp DNA linear PAT 10-JUL-2008

DEFINITION A novel immunosuppressive receptor.

ACCESSION DJ447641

VERSION DJ447641.1 GI:194091312

KEYWORDS JP 2004208583-A/2.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1997)

AUTHORS Takahashi,T., Manabe,T., Isogai,T., Sugiyama,T., Irie,R.,
 Wakamatsu,A., Ishii,S. and Sato,H.

TITLE A novel immunosuppressive receptor

JOURNAL Patent: JP 2004208583-A 2 29-JUL-2004;
 Mochida Pharmaceutical Co Ltd, Research Association for
 Biotechnology

COMMENT OS homo sapiens

PN JP 2004208583-A/2

PD 29-JUL-2004

PF 27-DEC-2002 JP 2002381558

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 sugiyama,

PI ryotaro irie,ai wakamatsu,shizuko ishii,hiroyuki sato CC

FH Key Location/Qualifiers.

FEATURES Location/Qualifiers

source 1..1997

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

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|------------------------|---------|---------------|-----|
| Length: | 1997 | | |
| Score: | 2302.00 | Matches: | 438 |
| Percent Similarity: | 99.3% | Conservative: | 1 |
| Best Local Similarity: | 99.1% | Mismatches: | 0 |
| Query Match: | 98.4% | Indels: | 3 |
| DB: | 9 | Gaps: | 1 |

US-10-574-045-4 (1-441) x DJ447641 (1-1997)

| | | | |
|----|-----|--|-----|
| Qy | 1 | MetLeuProSerLeuGlyProMetLeuLeuTrpThrAlaValLeuLeuPheValProCys | 20 |
| | | | |
| Db | 87 | ATGTTGCCATCTTTAGGCCCATGCTGCTCGGACGGCTGTGCTCTTTGTTCCCTGT | 146 |
| Qy | 21 | ValGlyLysThrValTrpLeuTyrLeuGlnAlaTrpProAsnProValPheGluGlyAsp | 40 |
| | | | |
| Db | 147 | GTTGGGAAACGTGTCTGGCTGTACTCCAGCCTGGCCAAACCTGTGTTGAAGGAGAT | 206 |
| Qy | 41 | AlaLeuThrLeuArgCysGlnGlyTrpLysAsnThrProLeuSerGlnValLysPheTyr | 60 |
| | | | |
| Db | 207 | GCCCTGACTCTGCGATGTCAGGGATGAAGAATACACCCTGCTCTCAGGTGAAGTTCTAC | 266 |
| Qy | 61 | ArgAspGlyLysPheLeuHisPheSerLysGluAsnGlnThrLeuSerMetGlyAlaAla | 80 |
| | | | |
| Db | 267 | AGAGATGGAAATTCCTTCAATTTCTCTAAGGAAACCACTCTGTCCATGGGAGCAGCA | 326 |
| Qy | 81 | ThrValGlnSerArgGlyGlnTyrSerCysSerGlyGlnValMetTyrIleProGlnThr | 100 |
| | | | |
| Db | 327 | ACAGTGCAGAGCCGTGGCAGTACAGCTGCTCTGGCAGGTGATGTATATCCACAGACA | 386 |
| Qy | 101 | PheThrGlnThrSerGluThrAlaMetValGlnValGlnGluLeuPheProProVal | 120 |
| | | | |
| Db | 387 | TTACACAAACTTCAGAGACTGCCATGGTTCAAGTCCAGAGCTGTTTCCACCTCCTGTG | 446 |
| Qy | 121 | LeuSerAlaIleProSerProGluProArgGluGlySerLeuValThrLeuArgCysGln | 140 |
| | | | |
| Db | 447 | CTGAGTGCCATCCCTCTCTGAGCCCCGAGAGGGTAGCCTGGTGAACCTGAGATGTCAG | 506 |
| Qy | 141 | ThrLysLeuHisProLeuArgSerAlaLeuArgLeuLeuPheSerPheHisLysAspGly | 160 |
| | | | |
| Db | 507 | ACAAAGCTGCACCCCTGAGGTGAGCTTGAGGCTCCTTTTCTCTTCCACAAGGAGCGC | 566 |
| Qy | 161 | HisThrLeuGlnAspArgGlyProHisProGluLeuCysIleProGlyAlaLysGluGly | 180 |
| | | | |
| Db | 567 | CACACCTTGCAGGACAGGGGCCCTCACCCAGAACTCTGCATCCCGGAGCCAAGGAGGGA | 626 |
| Qy | 181 | AspSerGlyLeuTyrTrpCysGluValAlaProGluGlyGlyGlnValGlnLysGlnSer | 200 |
| | | | |
| Db | 627 | GACTCTGGGCTTTACTGGTGTAGGTGGCCCTGAGGGTGGCCAGGTCCAGAAGCAGAGC | 686 |
| Qy | 201 | ProGlnLeuGluValArgValGlnAlaProValSerArgProValLeuThrLeuHisHis | 220 |
| | | | |
| Db | 687 | CCCCAGCTGGAGGTGAGAGTGCAGGCTCCTGTATCCCGTCTGTGCTCACTCTGCACCAC | 746 |

Qy 221 GlyProAlaAspProAlaValGlyAspMetValGlnLeuLeuCysGluAlaGlnArgGly 240
 |||
 Db 747 GGGCTGCTGACCTGCTGTGGGGACATGGTGACGCTCCTCTGTGAGGCACAGAGGGG 806

Qy 241 SerProProIleLeuTyrSerPheTyrLeuAspGluLysIleValGlyAsnHisSerAla 260
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 Db 807 TCCCTCCGATCCTGTATTCCTTCTACCTTGATGAGAAGATTGTGGGAACCACTCAGCT 866

Qy 261 ProCysGlyGlyThrThrSerLeuLeuPheProValLysSerGluGlnAspAlaGlyAsn 280
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 Db 867 CCCTGTGGTGAACCACTCCCTCCTCTCCAGTGAAGTCAGAACAGGATGCTGGGAAC 926

Qy 281 TyrSerCysGluAlaGluAsnSerValSerArgGluArgSerGluProLysLysLeuSer 300
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 Db 927 TACTCTCGAGGCTGAGAACAGTGTCTCCAGAGAGAGTGAAGCCCAAGAGCTGTCT 986

Qy 301 LeuLysGlySerGlnValLeuPheThrProAlaSerAsnTrpLeuValProTrpLeuPro 320
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 Db 987 CTGAAGGGTTCTCAAGTCTTGCTCACTCCGCCCACTGGCTGGTCTCTGGCTCTCT 1046

Qy 321 AlaSerLeuLeuGlyLeuMetValIleAlaAlaAlaLeuLeuValTyrValArgSerTrp 340
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 Db 1047 GCGAGCCTGCTTGGCTGATGGTTATGCTGCTGCACTTCTGGTTATGTGAGATCCTGG 1106

Qy 341 ArgLysAlaGlyProLeuProSerGlnIleProProThrAlaProGlyGlyGluGlnCys 360
 |||
 Db 1107 AGAAAAGCTGGGCCCTTCCATCCAGATACCACCACAGCTCCAGGTGGAGCAGTGC 1166

Qy 361 ProLeuTyrAlaAsnValHisHisGlnLysGlyLysAspGluGlyValValTyrSerVal 380
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 Db 1167 CCACATATAGCCAACGTGCATCACAGAAAGGGAAGATGAAGGTGTGTCTACTCTGTG 1226

Qy 381 ValHisArgThrSerLysArgSerGluAlaArgSerAlaGluPheThrVal-GlyArgLys 400
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 Db 1227 GTGCATAGAACCCTCAAAGAGGAGTGAAGCCAGGTCTGCTGAGTTACCGTGGGA----- 1281

Qy 400 sAspSerSerIleIleCysAlaGluValArgCysLeuGlnProSerGluValSerSerTh 420
 :::
 Db 1282 -GAAAGTTCTATCATCTGTGCGGAGGTGAGATGCCTGCAGCCAGTGAGGTTTCATCCAC 1340

Qy 420 rGluValAsnMetArgSerArgThrLeuGlnGluProLeuSerAspCysGluGluValLe 440
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 Db 1341 GGAGGTGAATATGAGAAGCAGGACTCTCCAGAAACCCCTTAGCGACTGTGAGGAGGTCT 1400

Qy 440 uCys 441
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 Db 1401 CTGC 1404

RESULT 6

AK131201

LOCUS

AK131201

1997 bp

mRNA

linear

PRI 09-JAN-2008